RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: _10/554,387_

Source: _PCT/IO_

Date Processed by STIC: _11/1/05_

ENTERED

CRF Errors Edited by the STIC Systems Branch

Serial Number: _10/554,387_   CRF Edit Date: _11/3/05_

Edited by: _____

____ Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line

____ Corrected the SEQ ID NO. Sequence numbers edited were:

_____

____ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

_____

_/__ Deleted: ___ invalid beginning/end-of-file text ; ___ page numbers

____ Inserted mandatory headings/numeric identifiers, specifically:

_____

____ Moved responses to same line as heading/numeric identifier, specifically:

_____

_/__ Other: _Sequence 8 - aligned amino acid number_

_____

_____

Revised 09/09/2003

PCT

RAW SEQUENCE LISTING   `   DATE: 11/03/2005
PATENT APPLICATION: US/10/554,387   TIME: 12:33:35

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF4\11032005\J554387.raw

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   3 <110> APPLICANT: Shaaltiel, Yoseph
   4       Baum, Gideon
   5       Sharon Hashmueli
   6       Ayala Lewkowicz
   7       Bartfeld, Daniel
   9 <120> TITLE OF INVENTION: PRODUCTION OF HIGH MANNOSE PROTEINS IN PLANT CULTURE
  11 <130> FILE REFERENCE: 30570
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/554,387
C--> 13 <141> CURRENT FILING DATE: 2005-10-25
  13 <160> NUMBER OF SEQ ID NOS: 14
  15 <170> SOFTWARE: PatentIn version 3.3
  17 <210> SEQ ID NO: 1
  18 <211> LENGTH: 22
  19 <212> TYPE: PRT
  20 <213> ORGANISM: Artificial sequence
  22 <220> FEATURE:
  23 <223> OTHER INFORMATION: ER signal peptide
  25 <400> SEQUENCE: 1
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  28 1               5                   10                  15
  31 Leu Ser Ser Ala Glu Phe
  32            20
  35 <210> SEQ ID NO: 2
  36 <211> LENGTH: 7
  37 <212> TYPE: PRT    ´
  38 <213> ORGANISM: Artificial sequence
  40 <220> FEATURE:
  41 <223> OTHER INFORMATION: Vacuolar targeting signal from Tobacco chitinase A
  43 <400> SEQUENCE: 2
  45 Asp Leu Leu Val Asp Thr Met
  46 1               5
  49 <210> SEQ ID NO: 3
  50 <211> LENGTH: 21
  51 <212> TYPE: DNA
  52 <213> ORGANISM: Artificial sequence
  54 <220> FEATURE:
  55 <223> OTHER INFORMATION: Single strand DNA oligonucleotide
  57 <400> SEQUENCE: 3
  58 cagaattcgc ccgcccctgc a                                          21
  61 <210> SEQ ID NO: 4
  62 <211> LENGTH: 22
  63 <212> TYPE: DNA
  64 <213> ORGANISM: Artificial sequence
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RAW SEQUENCE LISTING   DATE: 11/03/2005
PATENT APPLICATION: US/10/554,387   TIME: 12:33:35

Input Set : **A:\PTO.AMC.txt**
Output Set: **N:\CRF4\11032005\J554387.raw**

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 67 <223> OTHER INFORMATION: Single strand DNA oligonucleotide
 69 <400> SEQUENCE: 4
 70 ctcagatctt ggcgatgcca ca                                              22
 73 <210> SEQ ID NO: 5
 74 <211> LENGTH: 19
 75 <212> TYPE: DNA
 79 <213> ORGANISM: Artificial sequence
 81 <220> FEATURE:
 82 <223> OTHER INFORMATION: Single strand DNA oligonucleotide
 84 <400> SEQUENCE: 5
 85 ctcagaagac cagagggct                                                  19
 88 <210> SEQ ID NO: 6
 89 <211> LENGTH: 17
 90 <212> TYPE: DNA
 91 <213> ORGANISM: Artificial sequence
 93 <220> FEATURE:
 94 <223> OTHER INFORMATION: Single strand DNA oligonucleotide
 96 <400> SEQUENCE: 6
 97 caaagcggcc atcgtgc                                                    17
100 <210> SEQ ID NO: 7
101 <211> LENGTH: 1491
102 <212> TYPE: DNA
103 <213> ORGANISM: Homo sapiens
105 <400> SEQUENCE: 7
106 gcccgcccct gcatccctaa aagcttcggc tacagctcgg tggtgtgtgt ctgcaatgcc    60
108 acatactgtg actcctttga ccccccgacc tttcctgccc ttggtacctt cagccgctat   120
110 gagagtacac gcagtgggcg acggatggag ctgagtatgg ggcccatcca ggctaatcac   180
112 acgggcacag gcctgctact gaccctgcag ccagaacaga agttccagaa agtgaaggga   240
114 tttggagggg ccatgacaga tgctgctgct ctcaacatcc ttgccctgtc accccctgcc   300
116 caaaatttgc tacttaaatc gtacttctct gaagaaggaa tcggatataa catcatccgg   360
118 gtacccatgg ccagctgtga cttctccatc cgcacctaca cctatgcaga cacccctgat   420
120 gatttccagt tgcacaactt cagcctccca gaggaagata ccaagctcaa gatacccctg   480
122 attcaccgag ccctgcagtt ggcccagcgt cccgtttcac tccttgccag ccccctggaca   540
124 tcacccactt ggctcaagac caatggagcg gtgaatggga aggggtcact caagggacag   600
126 cccggagaca tctaccacca gacctgggcc agatactttg tgaagttcct ggatgcctat   660
128 gctgagcaca agttacagtt ctgggcagtg acagctgaaa atgagccttc tgctgggctg   720
130 ttgagtggat acccccttcca gtgcctgggc ttcaccccctg aacatcagcg agacttcatt   780
132 gcccgtgacc taggtcctac cctcgccaac agtactcacc acaatgtccg cctactcatg   840
134 ctggatgacc aacgcttgct gctgccccac tgggcaaagg tggtactgac agacccagaa   900
136 gcagctaaat atgttcatgg cattgctgta cattggtacc tggactttct ggctccagcc   960
138 aaagccaccc taggggagac acaccgcctg ttccccaaca ccatgctctt gcctcagag   1020
140 gcctgtgtgg gctccaagtt ctgggagcag agtgtgcggc taggctcctg ggatcgaggg  1080
142 atgcagtaca gccacagcat catcacgaac ctcctgtacc atgtggtcgg ctggaccgac  1140
144 tggaaccttg ccctgaaccc cgaaggagga cccaattggg tgcgtaactt tgtcgacagt  1200
146 cccatcattg tagacatcac caaggacacg ttttacaaac agcccatgtt ctaccacctt  1260
148 ggccacttca gcaagttcat tcctgagggc tcccagagag tggggctggt tgccagtcag  1320
150 aagaacgacc tggacgcagt ggcactgatg catcccgatg gctctgctgt tgtggtcgtg  1380
152 ctaaaccgct ccctctaagga tgtgcctctt accatcaagg atcctgctgt gggcttcctg  1440
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154 gagacaatct cacctggcta ctccattcac acctacctgt ggcatcgcca g   1491
157 <210> SEQ ID NO: 8
158 <211> LENGTH: 335
159 <212> TYPE: PRT
160 <213> ORGANISM: Homo sapiens
162 <400> SEQUENCE: 8
164 Ala Arg Pro Cys Ile Pro Lys Ser Phe Gly Tyr Ser Ser Val Val Cys
165 1   5   10   15
168 Val Cys Asn Ala Thr Tyr Cys Asp Ser Phe Asp Pro Pro Thr Phe Pro
169   20   25   30
172 Ala Leu Gly Thr Phe Ser Arg Tyr Glu Ser Thr Arg Ser Gly Arg Arg
173   35   40   45
176 Met Glu Leu Ser Met Gly Pro Ile Gln Ala Asn His Thr Gly Thr Gly
177   50   55   60
180 Leu Leu Leu Thr Leu Gln Pro Glu Gln Lys Phe Gln Lys Val Lys Gly
181 65   70   75   80
184 Phe Gly Gly Ala Met Thr Asp Ala Ala Ala Leu Asn Ile Leu Ala Leu
185   85   90   95
188 Ser Pro Pro Ala Gln Asn Leu Leu Leu Lys Ser Tyr Phe Ser Glu Glu
189   100   105   110
192 Gly Val Arg Leu Leu Met Leu Asn Asp Gln Arg Leu Leu Leu Pro His
193   ·   115   120   125
196 Trp Ala Lys Val Val Leu Thr Asp Pro Glu Ala Ala Lys Tyr Val His
197   130   135   140
200 Gly Ile Ala Val His Trp Tyr Leu Asp Phe Leu Ala Pro Ala Lys Ala
201 145   150   155   160
204 Thr Leu Gly Glu Thr His Arg Leu Phe Pro Asn Thr Met Leu Phe Ala
205   165   170   175
208 Ser Glu Ala Cys Val Gly Ser Lys Phe Trp Glu Gln Ser Val Arg Leu
209   180   185   190
212 Gly Ser Trp Asp Arg Gly Met Gln Tyr Ser His Ser Ile Ile Thr Asn
213   195   200   205
216 Leu Leu Tyr His Val Val Gly Trp Thr Asp Trp Asn Leu Ala Leu Asn
217   210   215   220
220 Pro Glu Gly Gly Pro Asn Trp Val Arg Asn Phe Val Asp Ser Pro Ile
221 225   230   235   240
224 Ile Val Asp Ile Thr Lys Asp Thr Phe Tyr Lys Gln Pro Met Phe Tyr
225   245   250   255
232 His Leu Gly His Phe Ser Lys Phe Ile Pro Glu Gly Ser Gln Arg Val
233   260   265   270
236 Gly Leu Val Ala Ser Gln Lys Asn Asp Leu Asp Ala Val Ala Leu Met
237   275   280   285
240 His Pro Asp Gly Ser Ala Val Val Val Leu Asn Arg Ser Ser Lys
241   290   295   300
244 Asp Val Pro Leu Thr Ile Lys Asp Pro Ala Val Gly Phe Leu Glu Thr
245 305   310   315   320
248 Ile Ser Pro Gly Tyr Ser Ile His Thr Tyr Leu Trp His Arg Gln
249   325   330   ·335
252 <210> SEQ ID NO: 9

RAW SEQUENCE LISTING   DATE: 11/03/2005
PATENT APPLICATION: US/10/554,387   TIME: 12:33:35

Input Set : **A:\PTO.AMC.txt**
Output Set: **N:\CRF4\11032005\J554387.raw**

```
253 <211> LENGTH: 338
254 <212> TYPE: DNA
255 <213> ORGANISM: Cauliflower mosaic virus
257 <400> SEQUENCE: 9
258 ttttcacaaa gggtaatatc gggaaacctc ctcggattcc attgcccagc tatctgtcac    60
260 ttcatcgaaa ggacagtaga aaaggaaggt ggctcctaca aatgccatca ttgcgataaa   120
262 ggaaaggcta tcgttcaaga tgcctctacc gacagtggtc ccaaagatgg acccccaccc   180
264 acgaggaaca tcgtggaaaa agaagacgtt ccaaccacgt cttcaaagca agtggattga   240
266 tgtgatatct ccactgacgt aagggatgac gcacaatccc actatccttc gcaagaccct   300
268 tcctctatat aaggaagttc atttcatttg gagaggac                           338
271 <210> SEQ ID NO: 10
272 <211> LENGTH: 66
273 <212> TYPE: DNA
274 <213> ORGANISM: Artificial sequence
276 <220> FEATURE:
277 <223> OTHER INFORMATION: Nucleic acid sequence encoding the ER signal peptide
279 <400> SEQUENCE: 10
280 atgaagacta atcttttct ctttctcatc ttttcacttc tcctatcatt atcctcggcc      60
282 gaattc                                                               66
285 <210> SEQ ID NO: 11
286 <211> LENGTH: 21
287 <212> TYPE: DNA
288 <213> ORGANISM: Artificial sequence
290 <220> FEATURE:
291 <223> OTHER INFORMATION: Nucleic acid sequence encoding the vacuolar targeting
sequence
293 <400> SEQUENCE: 11
294 gatcttttag tcgatactat g                                              21
297 <210> SEQ ID NO: 12
298 <211> LENGTH: 167
299 <212> TYPE: DNA
300 <213> ORGANISM: Artificial sequence
302 <220> FEATURE:
303 <223> OTHER INFORMATION: Nucleic acid sequence of the Agrobacterium tumefaciens
terminator
306 <220> FEATURE:
307 <221> NAME/KEY: misc_feature
308 <222> LOCATION: (162)..(162)
309 <223> OTHER INFORMATION: n is a, c, g, or t
311 <400> SEQUENCE: 12
312 taatttcatg atctgttttg ttgtattccc ttgcaatgca gggcctaggg ctatgaataa    60
314 agttaatgtg tgaatgtgtg aatgtgtgat tgtgacctga agggatcacg actataatcg   120
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W--> `316 tttataataa acaaagactt tgtcccaaaa accccccccc cngcaga                  167`
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319 <210> SEQ ID NO: 13
320 <211> LENGTH: 2186
321 <212> TYPE: DNA
322 <213> ORGANISM: Artificial sequence
324 <220> FEATURE:
325 <223> OTHER INFORMATION: nucleic acid sequence encoding high mannose human
326       glucocerebrosidase (GCD)
329 <220> FEATURE:
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RAW SEQUENCE LISTING   DATE: 11/03/2005
PATENT APPLICATION: US/10/554,387   TIME: 12:33:35

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF4\11032005\J554387.raw

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330 <221> NAME/KEY: misc_feature
331 <222> LOCATION: (2181)..(2181)
332 <223> OTHER INFORMATION: n is a, c, g, or t
334 <400> SEQUENCE: 13
335 ttttcacaaa gggtaatatc gggaaacctc ctcggattcc attgcccagc tatctgtcac      60
337 ttcatcgaaa ggacagtaga aaaggaaggt ggctcctaca aatgccatca ttgcgataaa     120
339 ggaaaggcta tcgttcaaga tgcctctacc gacagtggtc ccaaagatgg accccccaccc    180
341 acgaggaaca tcgtggaaaa agaagacgtt ccaaccacgt cttcaaagca agtggattga     240
343 tgtgatatct ccactgacgt aagggatgac gcacaatccc actatccttc gcaagaccct     300
345 tcctctatat aaggaagttc atttcatttg gagaggacag gcttcttgag atccttcaac     360
347 aattaccaac aacaacaaac aacaaacaac attacaatta ctatttacaa ttacagtcga     420
349 gggatccaag gagatataac aatgaagact aatcttttc tctttctcat cttttcactt      480
351 ctcctatcat tatcctcggc cgaattcgcc cgcccctgca tccctaaaag cttcggctac     540
353 agctcggtgg tgtgtgtctg caatgccaca tactgtgact cctttgaccc cccgaccttt     600
355 cctgcccttg gtaccttcag ccgctatgag agtacacgca gtgggcgacg gatggagctg     660
357 agtatggggc ccatccaggc taatcacacg ggcacaggcc tgctactgac cctgcagcca     720
359 gaacagaagt tccagaaagt gaagggattt ggaggggcca tgacagatgc tgctgctctc     780
361 aacatccttg ccctgtcacc ccctgcccaa aatttgctac ttaaatcgta cttctctgaa     840
363 gaaggaatcg gatataacat catccgggta cccatggcca gctgtgactt ctccatccgc     900
365 acctacacct atgcagacac ccctgatgat ttccagttgc acaacttcag cctcccagag     960
367 gaagatacca agctcaagat acccctgatt caccgagccc tgcagttggc ccagcgtccc    1020
369 gtttcactcc ttgccagccc ctggacatca cccacttggc tcaagaccaa tggagcggtg    1080
371 aatgggaagg ggtcactcaa gggacagccc ggagacatct accaccagac ctgggccaga    1140
373 tactttgtga agttcctgga tgcctatgct gagcacaagt tacagttctg ggcagtgaca    1200
380 gctgaaaatg agccttctgc tgggctgttg agtggatacc ccttccagtg cctgggcttc    1260
382 acccctgaac atcagcgaga cttcattgcc cgtgacctag gtcctaccct cgccaacagt    1320
384 actcaccaca atgtccgcct actcatgctg gatgaccaac gcttgctgct gccccactgg    1380
386 gcaaaggtgg tactgacaga cccagaagca gctaaatatg ttcatggcat tgctgtacat    1440
388 tggtacctgg actttctggc tccagccaaa gccaccctag gggagacaca ccgcctgttc    1500
390 cccaacacca tgctctttgc ctcagaggcc tgtgtgggct ccaagttctg ggagcagagt    1560
392 gtgcggctag gctcctggga tcgagggatg cagtacagcc acagcatcat cacgaacctc    1620
394 ctgtaccatg tggtcggctg gaccgactgg aaccttgccc tgaaccccga aggaggaccc    1680
396 aattgggtgc gtaactttgt cgacagtccc atcattgtag acatcaccaa ggacacgttt    1740
398 tacaaacagc ccatgttcta ccaccttggc cacttcagca gttcattcc tgagggctcc    1800
400 cagagagtgg ggctggttgc cagtcagaag aacgacctgg acgcagtggc actgatgcat    1860
402 cccgatggct ctgctgttgt ggtcgtgcta aaccgctcct ctaaggatgt gcctcttacc    1920
404 atcaaggatc ctgctgtggg cttcctggag acaatctcac ctggctactc cattcacacc    1980
406 tacctgtggc atcgccaaga tcttttagtc gatactatgt aatttcatga tctgttttgt    2040
408 tgtattccct tgcaatgcag ggcctagggc tatgaataaa gttaatgtgt gaatgtgtga    2100
410 atgtgtgatt gtgacctgaa gggatcacga ctataatcgt ttataataaa caaagacttt    2160
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415 <210> SEQ ID NO: 14
416 <211> LENGTH: 526
417 <212> TYPE: PRT
418 <213> ORGANISM: Artificial sequence
420 <220> FEATURE:
421 <223> OTHER INFORMATION: High mannose human glucocerebrosidase (GCD)
423 <400> SEQUENCE: 14
425 Met Lys Thr Asn Leu Phe Leu Phe Leu Ile Phe Ser Leu Leu Leu Ser
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 11/03/2005
PATENT APPLICATION: **US/10/554,387**   TIME: 12:33:36

Input Set : **A:\PTO.AMC.txt**
Output Set: **N:\CRF4\11032005\J554387.raw**

<u>Please Note:</u>
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:12; N Pos. 162
Seq#:13; N Pos. 2181

VERIFICATION SUMMARY   DATE: 11/03/2005
PATENT APPLICATION: US/10/554,387   TIME: 12:33:36

Input Set : **A:\PTO.AMC.txt**
Output Set: **N:\CRF4\11032005\J554387.raw**

L:13 M:270 C: Current Application Number differs, Replaced Current Application No
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:316 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:120
L:412 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:2160

Raw Sequence Listing before editing
(for reference only)

PCT

RAW SEQUENCE LISTING   DATE: 11/01/2005
PATENT APPLICATION: US/10/554,387   TIME: 11:00:57

Input Set : **A:\PTO.RJ.txt**
Output Set: **N:\CRF4\11012005\J554387.raw**

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 3 <110> APPLICANT: Shaaltiel, Yoseph
 4         Baum, Gideon
 5         Sharon Hashmueli
 6         Ayala Lewkowicz
 7         Bartfeld, Daniel
 9 <120> TITLE OF INVENTION: PRODUCTION OF HIGH MANNOSE PROTEINS IN PLANT CULTURE
11 <130> FILE REFERENCE: 30570
13 <140> CURRENT APPLICATION NUMBER: US/10/554,387
13 <141> CURRENT FILING DATE: 2005-10-25
13 <160> NUMBER OF SEQ ID NOS: 14
15 <170> SOFTWARE: PatentIn version 3.3
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C-->
C-->

ERRORED SEQUENCES

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162 <210> SEQ ID NO: 8
163 <211> LENGTH: 335
164 <212> TYPE: PRT
165 <213> ORGANISM: Homo sapiens
167 <400> SEQUENCE: 8
169 Ala Arg Pro Cys Ile Pro Lys Ser Phe Gly Tyr Ser Ser Val Val Cys
170 1               5                   10                  15
173 Val Cys Asn Ala Thr Tyr Cys Asp Ser Phe Asp Pro Pro Thr Phe Pro
174             20                  25                  30
177 Ala Leu Gly Thr Phe Ser Arg Tyr Glu Ser Thr Arg Ser Gly Arg Arg
178         35                  40                  45
181 Met Glu Leu Ser Met Gly Pro Ile Gln Ala Asn His Thr Gly Thr Gly
182     50                  55                  60
185 Leu Leu Leu Thr Leu Gln Pro Glu Gln Lys Phe Gln Lys Val Lys Gly
186 65                  70                  75                  80
189 Phe Gly Gly Ala Met Thr Asp Ala Ala Ala Leu Asn Ile Leu Ala Leu
190             85                  90                  95
193 Ser Pro Pro Ala Gln Asn Leu Leu Leu Lys Ser Tyr Phe Ser Glu Glu
194             100                 105                 110
197 Gly Val Arg Leu Leu Met Leu Asn Asp Gln Arg Leu Leu Leu Pro His
198         115                 120                 125
201 Trp Ala Lys Val Val Leu Thr Asp Pro Glu Ala Ala Lys Tyr Val His
202     130                 135                 140
205 Gly Ile Ala Val His Trp Tyr Leu Asp Phe Leu Ala Pro Ala Lys Ala
206 145                 150                 155                 160
209 Thr Leu Gly Glu Thr His Arg Leu Phe Pro Asn Thr Met Leu Phe Ala
210             165                 170                 175
213 Ser Glu Ala Cys Val Gly Ser Lys Phe Trp Glu Gln Ser Val Arg Leu
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RAW SEQUENCE LISTING   DATE: 11/01/2005
PATENT APPLICATION: US/10/554,387   TIME: 11:00:57

Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\11012005\J554387.raw

```
214             180                  185                  190
217 Gly Ser Trp Asp Arg Gly Met Gln Tyr Ser His Ser Ile Ile Thr Asn
218         195                  200                  205
221 Leu Leu Tyr His Val Val Gly Trp Thr Asp Trp Asn Leu Ala Leu Asn
222         210                  215                  220
225 Pro Glu Gly Gly Pro Asn Trp Val Arg Asn Phe Val Asp Ser Pro Ile
226 225                  230                  235                  240
229 Ile Val Asp Ile Thr Lys Asp Thr Phe Tyr Lys Gln Pro Met Phe Tyr
E--> 235    ·         245 245         ·    250 250    ·        255 255  ← misaligned
237 His Leu Gly His Phe Ser Lys Phe Ile Pro Glu Gly Ser Gln Arg Val     hos.
E--> 238         260                  265                  270
241 Gly Leu Val Ala Ser Gln Lys Asn Asp Leu Asp Ala Val Ala Leu Met
E--> 242         275                  280                  285
245 His Pro Asp Gly Ser Ala Val Val Val Val Leu Asn Arg Ser Ser Lys
E--> 246         290                  295                  300
249 Asp Val Pro Leu Thr Ile Lys Asp Pro Ala Val Gly Phe Leu Glu Thr
E--> 250 305                  310                  315                  320
253 Ile Ser Pro Gly Tyr Ser Ile His Thr Tyr Leu Trp His Arg Gln
E--> 254         325                  330                  335
426 <210> SEQ ID NO: 14
427 <211> LENGTH: 526
428 <212> TYPE: PRT
429 <213> ORGANISM: Artificial sequence     P3
431 <220> FEATURE:
432 <223> OTHER INFORMATION: High mannose human glucocerebrosidase (GCD)
434 <400> SEQUENCE: 14
436 Met Lys Thr Asn Leu Phe Leu Phe Leu Ile Phe Ser Leu Leu Leu Ser
437 1               5                  10                  15
440 Leu Ser Ser Ala Glu Phe Ala Arg Pro Cys Ile Pro Lys Ser Phe Gly
441         20                  25                  30
444 Tyr Ser Ser Val Val Cys Val Cys Asn Ala Thr Tyr Cys Asp Ser Phe
445         35                  40                  45
448 Asp Pro Pro Thr Phe Pro Ala Leu Gly Thr Phe Ser Arg Tyr Glu Ser
449         50                  55                  60
452 Thr Arg Ser Gly Arg Arg Met Glu Leu Ser Met Gly Pro Ile Gln Ala
453 65                  70                  75                  80
456 Asn His Thr Gly Thr Gly Leu Leu Leu Thr Leu Gln Pro Glu Gln Lys
457         85                  90                  95
460 Phe Gln Lys Val Lys Gly Phe Gly Gly Ala Met Thr Asp Ala Ala Ala
461         100                 105                 110
469 Leu Asn Ile Leu Ala Leu Ser Pro Pro Ala Gln Asn Leu Leu Leu Lys
470         115                 120                 125
473 Ser Tyr Phe Ser Glu Glu Gly Ile Gly Tyr Asn Ile Ile Arg Val Pro
474         130                 135                 140
477 Met Ala Ser Cys Asp Phe Ser Ile Arg Thr Tyr Thr Tyr Ala Asp Thr
478 145                 150                 155                 160
481 Pro Asp Asp Phe Gln Leu His Asn Phe Ser Leu Pro Glu Glu Asp Thr
482         165                 170                 175
485 Lys Leu Lys Ile Pro Leu Ile His Arg Ala Leu Gln Leu Ala Gln Arg
```

RAW SEQUENCE LISTING   DATE: 11/01/2005
PATENT APPLICATION: US/10/554,387   TIME: 11:00:57

Input Set : **A:\PTO.RJ.txt**
Output Set: **N:\CRF4\11012005\J554387.raw**

```
486           180                 185                 190
489 Pro Val Ser Leu Leu Ala Ser Pro Trp Thr Ser Pro Thr Trp Leu Lys
490           195                 200                 205
493 Thr Asn Gly Ala Val Asn Gly Lys Gly Ser Leu Lys Gly Gln Pro Gly
494           210                 215                 220
497 Asp Ile Tyr His Gln Thr Trp Ala Arg Tyr Phe Val Lys Phe Leu Asp
498 225                 230                 235                 240
501 Ala Tyr Ala Glu His Lys Leu Gln Phe Trp Ala Val Thr Ala Glu Asn
502               245                 250                 255
505 Glu Pro Ser Ala Gly Leu Leu Ser Gly Tyr Pro Phe Gln Cys Leu Gly
506           260                 265                 270
509 Phe Thr Pro Glu His Gln Arg Asp Phe Ile Ala Arg Asp Leu Gly Pro
510           275                 280                 285
513 Thr Leu Ala Asn Ser Thr His His Asn Val Arg Leu Leu Met Leu Asp
514       290                 295                 300
517 Asp Gln Arg Leu Leu Leu Pro His Trp Ala Lys Val Val Leu Thr Asp
518 305                 310                 315                 320
521 Pro Glu Ala Ala Lys Tyr Val His Gly Ile Ala Val His Trp Tyr Leu
522               325                 330                 335
525 Asp Phe Leu Ala Pro Ala Lys Ala Thr Leu Gly Glu Thr His Arg Leu
526           340                 345                 350
529 Phe Pro Asn Thr Met Leu Phe Ala Ser Glu Ala Cys Val Gly Ser Lys
·530           355                 360                 365
533 Phe Trp Glu Gln Ser Val Arg Leu Gly Ser Trp Asp Arg Gly Met Gln
534       370                 375                 380
537 Tyr Ser His Ser Ile Ile Thr Asn Leu Leu Tyr His Val Val Gly Trp
538 385                 390                 395                 400
541 Thr Asp Trp Asn Leu Ala Leu Asn Pro Glu Gly Gly Pro Asn Trp Val
542           405                 410                 415
548 Arg Asn Phe Val Asp Ser Pro Ile Ile Val Asp Ile Thr Lys Asp Thr
549           420                 425                 430
552 Phe Tyr Lys Gln Pro Met Phe Tyr His Leu Gly His Phe Ser Lys Phe
553       435                 440                 445
556 Ile Pro Glu Gly Ser Gln Arg Val Gly Leu Val Ala Ser Gln Lys Asn
557       450                 455                 460
560 Asp Leu Asp Ala Val Ala Leu Met His Pro Asp Gly Ser Ala Val Val
561 465                 470                 475                 480
564 Val Val Leu Asn Arg Ser Ser Lys Asp Val Pro Leu Thr Ile Lys Asp
565           485                 490                 495
568 Pro Ala Val Gly Phe Leu Glu Thr Ile Ser Pro Gly Tyr Ser Ile His
569           500                 505                 510
572 Thr Tyr Leu Trp His Arg Gln Asp Leu Leu Val Asp Thr Met
573           515                 520                 525
```

E--> 580 12
E--> 582 2
E--> 585 pcdo
E--> 588 12022/ph/00

VERIFICATION SUMMARY   DATE: 11/01/2005
PATENT APPLICATION: US/10/554,387   TIME: 11:00:58

Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\11012005\J554387.raw

```
L:13  M:270 C: Current Application Number differs, Replaced Current Application No
L:13  M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:235 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:8
L:238 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:8
L:242 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:8
L:246 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:8
L:250 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:8
L:254 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:8
L:327 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:120
L:423 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:2160
L:580 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:14
L:582 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:14
L:585 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:585 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
L:588 M:252 E: No. of Seq. differs, <211> LENGTH:Input:526 Found:527 SEQ:14
```